

AMENDMENTS TO CLAIMS

Claims 1-29 (canceled).

30. (New) A method of identifying endogenous mRNA subsets in a cell, comprising the steps of:
- (a) lysing a cell comprising an mRNA-protein (mRNP) complex;
 - (b) contacting the mRNP complex with an antibody that specifically binds at least one component of the mRNP complex;
 - (c) partitioning the mRNP complex by capturing the antibody on a solid support;
 - (d) removing the mRNP complex from the solid support; and
 - (e) identifying a plurality of mRNAs from the mRNP complex without amplifying the mRNAs by PCR, thereby to produce a gene expression profile comprising the identity of the mRNAs in the mRNP complex.
31. (New) The method of claim 30, wherein the plurality of mRNAs are reverse transcribed prior to their identification.
32. (New) The method of claim 30, wherein the plurality of mRNAs are identified using hybridization.
33. (New) The method of claim 30, wherein the plurality of mRNAs are identified by sequencing.
34. (New) The method of claim 30, wherein the plurality of mRNAs are identified using a microarray.
35. (New) The method of claim 34, wherein the microarray is a cDNA array.
36. (New) The method of claim 30, wherein the method does not include iterative selection prior to the identification of the mRNAs.
37. (New) The method of claim 30, wherein the component of the mRNP complex to which the antibody binds is an endogenous RNA-binding protein.
38. (New) The method of claim 37, wherein the endogenous RNA-binding protein is polyA-binding protein (PABP).

39. (New) The method of claim 30, wherein the mRNP protein is partitioned from a cell lysate.
40. (New) The method of claim 30, further comprising identifying changes in the endogenous RNA subsets following treatment of the cell with a drug.
41. (New) The method of claim 30, further comprising identifying changes in the endogenous RNA subsets during cell cycle, developmental events, or a state of ageing.
42. (New) The method of claim 30, wherein the cell is a tumor cell.
43. (New) The method of claim 30, wherein the cell is an animal or plant cell.
44. (New) The method of claim 30, wherein the cell is infected with a pathogen.
45. (New) The method of claim 30, wherein the RNA-binding protein is tissue-specific.
46. (New) The method of claim 30, wherein the plurality of mRNAs are identified *en masse*.
47. (New) The method of claim 30, wherein the plurality of mRNAs comprises approximately 10% of total mRNAs.
48. (New) A method of identifying endogenous mRNA subsets in a cell, comprising the steps of:
 - (a) contacting an mRNP complex with an epitope-tagged RNA-binding protein or an epitope-tagged RNA-associated protein (RAP) ectopically expressed in a cell;
 - (b) lysing the cell;
 - (c) partitioning the mRNP complex by capturing the RNA binding protein or the RAP on a solid support;
 - (d) removing the mRNP complex from the solid support; and
 - (e) identifying a plurality of mRNAs from the mRNP complex without amplifying the mRNAs by PCR, thereby to produce a gene expression profile comprising the identity of the mRNAs in the mRNP complex.
49. (New) The method of claim 48, wherein the plurality of mRNAs are reverse transcribed prior to their identification.

50. (New) The method of claim 48, wherein the plurality of mRNAs are identified using hybridization.
51. (New) The method of claim 48, wherein the plurality of mRNAs are identified by sequencing.
52. (New) The method of claim 48, wherein the plurality of mRNAs are identified using a microarray.
53. (New) The method of claim 52, wherein the microarray is a cDNA array.
54. (New) The method of claim 48, wherein the method does not include iterative selection prior to the identification of the mRNAs.
55. (New) The method of claim 48, wherein the epitope-tagged RNA-binding protein is ELAV/Hu protein.
56. (New) The method of claim 55, wherein the epitope-tagged RNA-binding protein is HuA or HuB.
57. (New) The method of claim 48, wherein the epitope tag is a bacteriophage gene-10 tag.
58. (New) The method of claim 48, wherein the mRNP complex is contacted with the epitope-tagged RNA-binding protein.
59. (New) The method of claim 48, further comprising identifying changes in the endogenous RNA subsets following treatment of the cell with a drug.
60. (New) The method of claim 48, further comprising identifying changes in the endogenous RNA subsets during cell cycle, developmental events, or a state of ageing.
61. (New) The method of claim 48, wherein the cell is a tumor cell.
62. (New) The method of claim 48, wherein the cell is an animal or plant cell.
63. (New) The method of claim 48, wherein the cell is infected with a pathogen.
64. (New) The method of claim 48, wherein the RNA-binding protein or the RAP is tissue-specific.
65. (New) The method of claim 48, wherein the plurality of mRNAs are identified *en masse*.

66. (New) The method of claim 48, wherein the plurality of mRNAs comprises approximately 10% of total mRNAs.